

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/806,852

Source: \_\_\_\_\_

Date Processed by STIC: \_\_\_\_\_

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 12/03/2004

PATENT APPLICATION: US/10/806,852

TIME: 07:22:53

Input Set : N:\Crf3\RULE60\10806852.raw.txt

Output Set: N:\CRF4\12032004\J806852.raw

## SEQUENCE LISTING

```

3 (1) GENERAL INFORMATION:
5     (i) APPLICANT: RUEGER, DAVID C.
6         SAMPATH, KUBER T.
7         OPPERMANN, HERMANN
8         PANG, ROY H.L.
9         COHEN, CHARLES M.
11    (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
12         TREATMENT OF MOTOR NEURON INJURY AND NEUROPATHY
14    (iii) NUMBER OF SEQUENCES: 9
16    (iv) CORRESPONDENCE ADDRESS:
17        (A) ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
18            THIBEAULT, LLP
19        (B) STREET: 125 HIGH STREET
20        (C) CITY: BOSTON
21        (D) STATE: MA
22        (E) COUNTRY: USA
23        (F) ZIP: 02110
25    (v) COMPUTER READABLE FORM:
26        (A) MEDIUM TYPE: Floppy disk
27        (B) COMPUTER: IBM PC compatible
28        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
31    (vi) CURRENT APPLICATION DATA:
C--> 37        (A) APPLICATION NUMBER: US/10/806,852
C--> 38        (B) FILING DATE: 23-Mar-2004
34        (C) CLASSIFICATION: 435
36    (viii) ATTORNEY/AGENT INFORMATION:
39        (A) NAME: MEYERS, THOMAS C.
40        (B) REGISTRATION NUMBER: 36,989
41        (C) REFERENCE/DOCKET NUMBER: CRP-155
43    (ix) TELECOMMUNICATION INFORMATION:
44        (A) TELEPHONE: (617) 248-7013
45        (B) TELEFAX: (617) 248-7100
48 (2) INFORMATION FOR SEQ ID NO: 1:
50    (i) SEQUENCE CHARACTERISTICS:
51        (A) LENGTH: 1822 base pairs
52        (B) TYPE: nucleic acid
53        (C) STRANDEDNESS: single
54        (D) TOPOLOGY: linear
56    (ii) MOLECULE TYPE: cDNA
58    (vi) ORIGINAL SOURCE:
59        (A) ORGANISM: HOMO SAPIENS

```

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60      (F) TISSUE TYPE: HIPPOCAMPUS
62      (ix) FEATURE:
63          (A) NAME/KEY: CDS
64          (B) LOCATION: 49..1341
65          (C) IDENTIFICATION METHOD: experimental
66          (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
67 /product= "OP1"
68 /evidence= EXPERIMENTAL
69 /standard_name= "OP1"
72      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
74 GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG      57
75                                         Met His Val
76                                         1
78 CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA      105
79 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
80      5      10      15
82 CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC      153
83 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
84 20      25      30      35
86 GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG      201
87 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
88      40      45      50
90 CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC      249
91 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
92      55      60      65
94 CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG      297
95 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
96      70      75      80
98 CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC      345
99 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
100      85      90      95
102 GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC      393
103 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
104 100      105      110      115
106 CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC      441
107 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
108      120      125      130
110 ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC      489
111 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe
112      135      140      145
114 CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC      537
115 His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile
116      150      155      160
118 CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC      585
119 Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp
120      165      170      175
122 TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT      633
123 Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr
124 180      185      190      195

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126	CAG	GTG	CTC	CAG	GAG	CAC	TTG	GGC	AGG	GAA	TCG	GAT	CTC	TTC	CTG	CTC	681
127	Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	
128				200						205					210		
130	GAC	AGC	CGT	ACC	CTC	TGG	GCC	TCG	GAG	GAG	GGC	TGG	CTG	GTG	TTT	GAC	729
131	Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	
132				215					220						225		
134	ATC	ACA	GCC	ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAT	CCG	CGG	CAC	AAC	CTG	777
135	Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	
136				230					235						240		
138	GGC	CTG	CAG	CTC	TCG	GTG	GAG	ACG	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	825
139	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	
140				245					250						255		
142	AAG	TTG	GCG	GGC	CTG	ATT	GGG	CGG	CAC	GGG	CCC	CAG	AAC	AAG	CAG	CCC	873
143	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	
144	260					265					270					275	
146	TTC	ATG	GTG	GCT	TTC	AAG	GCC	ACG	GAG	GTC	CAC	TTC	CGC	AGC	ATC		921
147	Phe	Met	Val	Ala	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	Arg	Ser	Ile		
148					280					285					290		
150	CGG	TCC	ACG	GGG	AGC	AAA	CAG	CGC	AGC	CAG	AAC	CGC	TCC	AAG	ACG	CCC	969
151	Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	
152				295						300					305		
154	AAG	AAC	CAG	GAA	GCC	CTG	CGG	ATG	GCC	AAC	GTG	GCA	GAG	AAC	AGC	AGC	1017
155	Lys	Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	
156				310					315						320		
158	AGC	GAC	CAG	AGG	CAG	GCC	TGT	AAG	AAG	CAC	GAG	CTG	TAT	GTC	AGC	TTC	1065
159	Ser	Asp	Gln	Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	
160				325					330						335		
162	CGA	GAC	CTG	GGC	TGG	CAG	GAC	TGG	ATC	ATC	GCG	CCT	GAA	GGC	TAC	GCC	1113
163	Arg	Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	
164	340					345					350					355	
166	GCC	TAC	TAC	TGT	GAG	GGG	GAG	TGT	GCC	TTC	CCT	CTG	AAC	TCC	TAC	ATG	1161
167	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	
168					360						365					370	
170	AAC	GCC	ACC	AAC	CAC	GCC	ATC	GTG	CAG	ACG	CTG	GTC	CAC	TTC	ATC	AAC	1209
171	Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn	
172				375						380					385		
174	CCG	GAA	ACG	GTG	CCC	AAG	CCC	TGC	TGT	GCG	CCC	ACG	CAG	CTC	AAT	GCC	1257
175	Pro	Glu	Thr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala	
176				390					395						400		
178	ATC	TCC	GTC	CTC	TAC	TTC	GAT	GAC	AGC	TCC	AAC	GTC	ATC	CTG	AAG	AAA	1305
179	Ile	Ser	Val	Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	
180				405					410						415		
182	TAC	AGA	AAC	ATG	GTG	GTC	CGG	GCC	TGT	GGC	TGC	CAC	TAGCTCCTCC				1351
183	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala	Cys	Gly	Cys	His					
184	420					425					430						
186	GAGAATTCAG	ACCCTTTGGG	GCCAAGTTTT	TCTGGATCCT	CCATTGCTCG	CCTTGGCCAG											1411
188	GAACCAGCAG	ACCAACTGCC	TTTTGTGAGA	CCTTCCCCTC	CCTATCCCCA	ACTTTAAAGG											1471
190	TGTGAGAGTA	TTAGGAAACA	TGAGCAGCAT	ATGGCTTTTG	ATCAGTTTTT	CAGTGGCAGC											1531
192	ATCCAATGAA	CAAGATCCTA	CAAGCTGTGC	AGGCAAAACC	TAGCAGGAAA	AAAAAACAAC											1591

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194 GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT 1651
196 CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711
198 GCGGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC 1771
200 CTGTAATAAA TGTCACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A 1822
203 (2) INFORMATION FOR SEQ ID NO: 2:
205     (i) SEQUENCE CHARACTERISTICS:
206         (A) LENGTH: 431 amino acids
207         (B) TYPE: amino acid
208         (D) TOPOLOGY: linear
210     (ii) MOLECULE TYPE: protein
212     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
214 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
215   1           5           10           15
217 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
218           20           25           30
220 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
221           35           40           45
223 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
224           50           55           60
226 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
227   65           70           75           80
229 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
230           85           90           95
232 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
233           100          105          110
235 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
236           115          120          125
238 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
239           130          135          140
241 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
242 145          150          155          160
244 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
245           165          170          175
247 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
248           180          185          190
250 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
251           195          200          205
253 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
254           210          215          220
256 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
257 225          230          235          240
259 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
260           245          250          255
262 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
263           260          265          270
265 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
266           275          280          285
268 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
269           290          295          300

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271 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
272 305                      310                      315                      320
274 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
275                      325                      330                      335
277 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
278                      340                      345                      350
280 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
281                      355                      360                      365
283 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
284                      370                      375                      380
286 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
287 385                      390                      395                      400
289 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
290                      405                      410                      415
292 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
293                      420                      425                      430

```

295 (2) INFORMATION FOR SEQ ID NO: 3:

297 (i) SEQUENCE CHARACTERISTICS:

298 (A) LENGTH: 102 amino acids

299 (B) TYPE: amino acid

300 (C) STRANDEDNESS:

301 (D) TOPOLOGY: linear

303 (ii) MOLECULE TYPE: protein

306 (ix) FEATURE:

307 (A) NAME/KEY: Protein

308 (B) LOCATION: 1..102

309 (D) OTHER INFORMATION: /label= OPX

310 /note= "wherein each Xaa is independently selected from a group

311 of one or more specified amino acids as defined in the

312 specification."

315 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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W--> 317 Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
318 1 5 10 15
320 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
321 20 25 30
323 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
324 35 40 45
326 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
327 50 55 60
329 Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
330 65 70 75 80
332 Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
333 85 90 95
335 Xaa Ala Cys Gly Cys His
336 100

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338 (2) INFORMATION FOR SEQ ID NO: 4:

340 (i) SEQUENCE CHARACTERISTICS:

341 (A) LENGTH: 97 amino acids

342 (B) TYPE: amino acid

## RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : N:\Crif3\RULE60\10806852.raw.txt

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos.2,3,9,11,16,19,23,26,35,39,41,50,52,56,57,58,60,61,65,71,73  
Seq#:3; Xaa Pos.75,80,82,84,87,89,91,97  
Seq#:4; Xaa Pos.2,3,4,6,7,8,11,12,13,14,15,16,18,19,20,21,23,26,28,30,31,33  
Seq#:4; Xaa Pos.34,35,36,37,38,39,40,44,45,46,47,48,49,50,51,52,53,54,55,56  
Seq#:4; Xaa Pos.57,58,59,60,63,65,66,67,68,69,70,71,72,74,75,76,77,78,79,80  
Seq#:4; Xaa Pos.82,84,85,86,87,88,90,92,93,95,97  
Seq#:5; Xaa Pos.2,3,4,5,7,8,9,11,12,13,16,17,18,19,20,21,23,24,25,26,28,31  
Seq#:5; Xaa Pos.33,35,36,38,39,40,41,42,43,44,45,49,50,51,52,53,54,55,56,57  
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Seq#:5; Xaa Pos.82,83,84,85,87,89,90,91,92,93,95,97,98,100,102  
Seq#:6; Xaa Pos.1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,18,19,20,21,22,23,24  
Seq#:6; Xaa Pos.26,28,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47  
Seq#:6; Xaa Pos.48,49,50,51,52,53,54,55,56,57,58,59,60,61,63,65,66,67,68,69  
Seq#:6; Xaa Pos.70,71,72,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90  
Seq#:6; Xaa Pos.91,92,93,95,97  
Seq#:7; Xaa Pos.2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,23,24  
Seq#:7; Xaa Pos.25,26,27,28,29,31,33,35,36,37,38,39,40,41,42,43,44,45,46,47  
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Seq#:7; Xaa Pos.70,71,72,73,74,75,76,77,79,80,81,82,83,84,85,86,87,88,89,90  
Seq#:7; Xaa Pos.91,92,93,94,95,96,97,98,100,102  
Seq#:8; Xaa Pos.2,3,4,5  
Seq#:9; Xaa Pos.2,3,4,5

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/806,852

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Input Set : N:\Crf3\RULE60\10806852.raw.txt

Output Set: N:\CRF4\12032004\J806852.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:37 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:37 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vi)  
L:38 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
M:341 Repeated in SeqNo=3  
L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
M:341 Repeated in SeqNo=4  
L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
M:341 Repeated in SeqNo=5  
L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
M:341 Repeated in SeqNo=6  
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0  
M:341 Repeated in SeqNo=7  
L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0  
L:555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0